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<b>Author(s)</b>	Mancabelli, Leonardo; Milani, Christian; Lugli, Gabriele A.; Turrone, Francesca; Mangifesta, Marta; Viappiani, Alice; Ticinesi, Andrea; Nouvenne, Antonio; Meschi, Tiziana; van Sinderen, Douwe; Ventura, Marco
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**University College Cork, Ireland**  
Coláiste na hOllscoile Corcaigh



**Unveiling the gut microbiota composition and functionality associated with constipation  
through metagenomic analyses**

Leonardo Mancabelli<sup>1</sup>, Christian Milani<sup>1</sup>, Gabriele Andrea Lugli<sup>1</sup>, Francesca Turrone<sup>1</sup>, Marta Mangifesta<sup>1,2</sup>, Alice Viappiani<sup>2</sup>, Andrea Ticinesi<sup>3</sup>, Antonio Nouvenne<sup>3</sup>, Tiziana Meschi<sup>3</sup>, Douwe van Sinderen<sup>4</sup> and Marco Ventura<sup>1</sup>

**Supplementary information**

## **Additional files**

**Figure S1.** Microbial profiling of the 147 samples at phylum level.

**Figure S2.** Evaluation of batch effects and age incidence on microbiota composition.

**Table S1.** Fecal samples collected in this study.

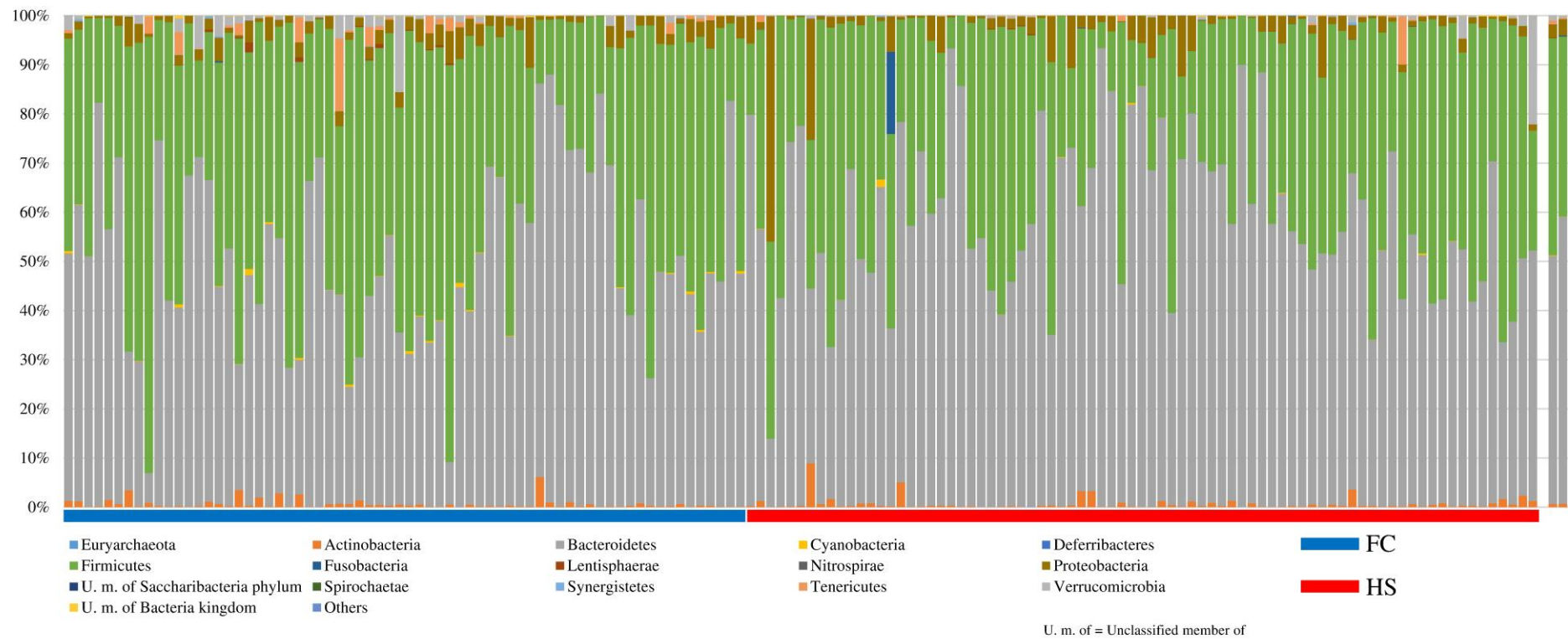
**Table S2.** Evaluation of homogeneity of the samples collected in this study.

**Table S3.** 16S rRNA microbial profiling data.

**Table S4.** Taxonomic profiling of the 147 analyzed samples at genus level.

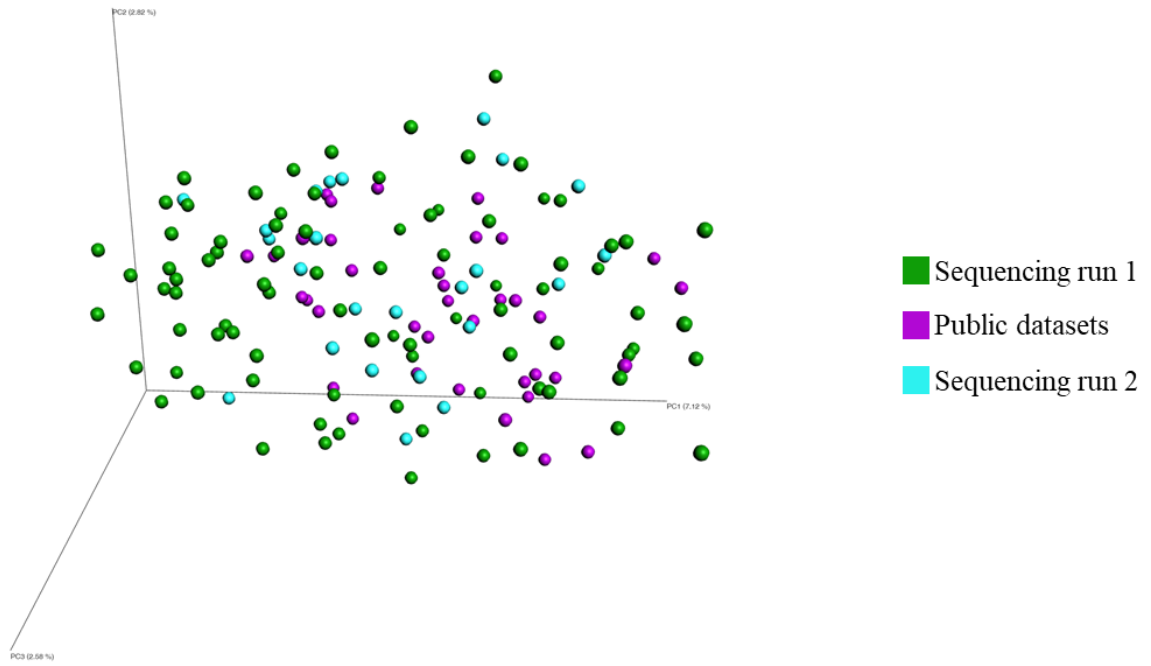
**Table S5.** Shotgun metagenomic data.

**Table S6.** List of pathways detected in analysis with a significant difference (p-value < 0.05).

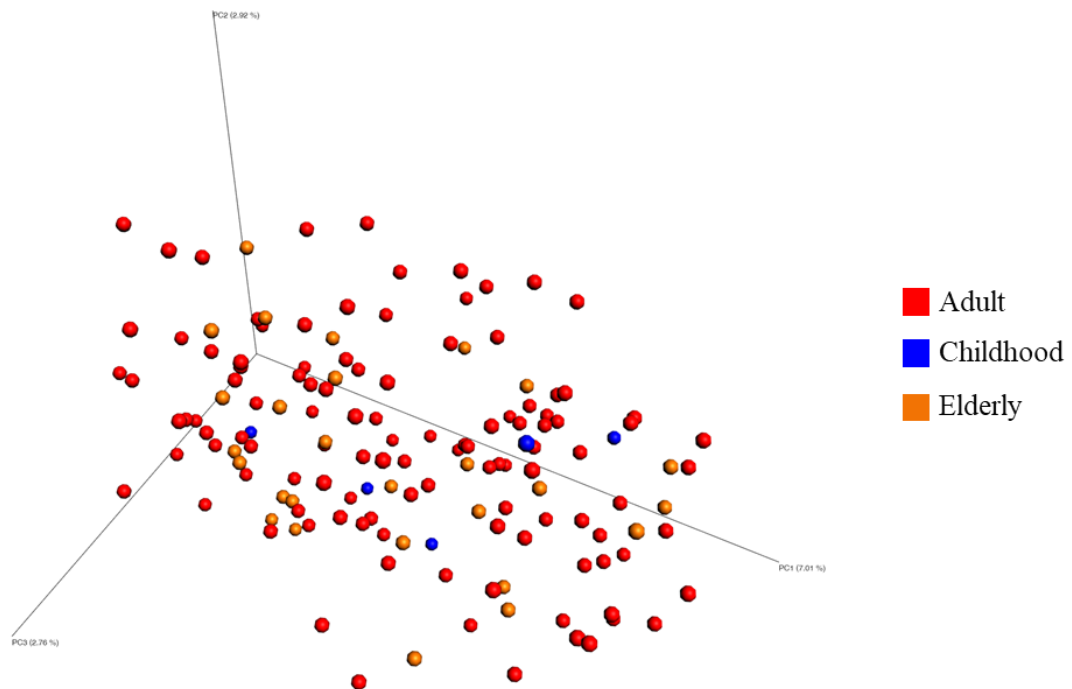


**Figure S1**

**a**



**b**



**Figure S2**